OIPE

Input Set: **I457066.RAW**

ENTERED

This Raw Listing contains the General Information Section and up to first 5 pages.

```
1    <110> APPLICANT: Gao, Zeren
2          Hart, Charles E.
3          Piddington, Christopher S.
4          Sheppard, Paul O.
5          Shoemaker, Kimberly E.
6          Gilbertson, Debra G.
7          West, James W.
8    <120> TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
9    <130> FILE REFERENCE: 98-60
10   <140> CURRENT APPLICATION NUMBER: US/09/457,066
11   <141> CURRENT FILING DATE: 1999-12-07
12   <160> NUMBER OF SEQ ID NOS: 50
13   <170> SOFTWARE: FastSEQ for Windows Version 3.0
14   <210> SEQ ID NO 1
15   <211> LENGTH: 1760
16   <212> TYPE: DNA
17   <213> ORGANISM: Homo sapiens
18   <220> FEATURE:
19   <221> NAME/KEY: CDS
20   <222> LOCATION: (154)...(1191)
21   <400> SEQUENCE: 1
22         attatgtgga aactaccctg cgattctctg ctgccagagc aggctcggcg cttccacccc    60
23         agtgcagcct tcccctggcg gtggtgaaag agactcggga gtcgctgctt ccaaagtgcc   120
24         cgccgtgagt gagctctcac cccagtcagc caa atg agc ctc ttc ggg ctt ctc    174
25                                                 Met Ser Leu Phe Gly Leu Leu
26                                                  1               5
27         ctg ctg aca tct gcc ctg gcc ggc cag aga cag ggg act cag gcg gaa    222
28         Leu Leu Thr Ser Ala Leu Ala Gly Gln Arg Gln Gly Thr Gln Ala Glu
29                  10                  15                  20
30         tcc aac ctg agt agt aaa ttc cag ttt tcc agc aac aag gaa cag aac    270
31         Ser Asn Leu Ser Ser Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn
32              25                  30                  35
33         gga gta caa gat cct cag cat gag aga att att act gtg tct act aat    318
34         Gly Val Gln Asp Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn
35           40                  45                  50                  55
36         gga agt att cac agc cca agg ttt cct cat act tat cca aga aat acg    366
37         Gly Ser Ile His Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr
38                      60                  65                  70
39         gtc ttg gta tgg aga tta gta gca gta gag gaa aat gta tgg ata caa    414
40         Val Leu Val Trp Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln
41                      75                  80                  85
42         ctt acg ttt gat gaa aga ttt ggg ctt gaa gac cca gaa gat gac ata    462
43         Leu Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile
44                  90                  95                  100
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45        tgc aag tat gat ttt gta gaa gtt gag gaa ccc agt gat gga act ata        510
46        Cys Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile
47            105                     110                 115
48        tta ggg cgc tgg tgt ggt tct ggt act gta cca gga aaa cag att tct        558
49        Leu Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser
50            120                 125                 130                 135
51        aaa gga aat caa att agg ata aga ttt gta tct gat gaa tat ttt cct        606
52        Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro
53                            140                 145                 150
54        tct gaa cca ggg ttc tgc atc cac tac aac att gtc atg cca caa ttc        654
55        Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe
56                        155                 160                 165
57        aca gaa gct gtg agt cct tca gtg cta ccc cct tca gct ttg cca ctg        702
58        Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu
59            170                 175                 180
60        gac ctg ctt aat aat gct ata act gcc ttt agt acc ttg gaa gac ctt        750
61        Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu
62            185                 190                 195
63        att cga tat ctt gaa cca gag aga tgg cag ttg gac tta gaa gat cta        798
64        Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu
65            200                 205                 210                 215
66        tat agg cca act tgg caa ctt ctt ggc aag gct ttt gtt ttt gga aga        846
67        Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Val Phe Gly Arg
68                        220                 225                 230
69        aaa tcc aga gtg gtg gat ctg aac ctt cta aca gag gag gta aga tta        894
70        Lys Ser Arg Val Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu
71                        235                 240                 245
72        tac agc tgc aca cct cgt aac ttc tca gtg tcc ata agg gaa gaa cta        942
73        Tyr Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu
74                        250                 255                 260
75        aag aga acc gat acc att ttc tgg cca ggt tgt ctc ctg gtt aaa cgc        990
76        Lys Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg
77                        265                 270                 275
78        tgt ggt ggg aac tgt gcc tgt tgt ctc cac aat tgc aat gaa tgt caa        1038
79        Cys Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln
80            280                 285                 290                 295
81        tgt gtc cca agc aaa gtt act aaa aaa tac cac gag gtc ctt cag ttg        1086
82        Cys Val Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu
83                        300                 305                 310
84        aga cca aag acc ggt gtc agg gga ttg cac aaa tca ctc acc gac gtg        1134
85        Arg Pro Lys Thr Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val
86                        315                 320                 325
87        gcc ctg gag cac cat gag gag tgt gac tgt gtg tgc aga ggg agc aca        1182
88        Ala Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr
89                        330                 335                 340
90        gga gga tag ccgcatcacc accagcagct cttgcccaga gctgtgcagt             1231
W-->  91        Gly Gly
92                        345
93        gcagtggctg attctattag agaacgtatg cgttatctcc atccttaatc tcagttgttt  1291
94        gcttcaagga cctttcatct tcaggattta cagtgcattc tgaaagagga gacatcaaac  1351
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 95          agaattagga gttgtgcaac agctcttttg agaggaggcc taaaggacag gagaaaaggt          1411
 96          cttcaatcgt ggaaagaaaa ttaaatgttg tattaaatag atcaccagct agtttcagag          1471
 97          ttaccatgta cgtattccac tagctgggtt ctgtatttca gttctttcga tacggcttag          1531
 98          ggtaatgtca gtacaggaaa aaaactgtgc aagtgagcac ctgattccgt tgccttgctt          1591
 99          aactctaaag ctccatgtcc tgggcctaaa atcgtataaa atctggattt tttttttttt          1651
100          ttttgctca tattcacata tgtaaaccag aacattctat gtactacaaa cctggttttt          1711
101          aaaaaggaac tatgttgcta tgaattaaac ttgtgtcgtg ctgatagga          1760
102     <210> SEQ ID NO 2
103     <211> LENGTH: 345
104     <212> TYPE: PRT
105     <213> ORGANISM: Homo sapiens
106     <400> SEQUENCE: 2
107          Met Ser Leu Phe Gly Leu Leu Leu Leu Thr Ser Ala Leu Ala Gly Gln
108          1               5                   10                  15
109          Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe
110                      20                  25                  30
111          Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
112                      35                  40                  45
113          Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
114              50                  55                  60
115          His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
116          65                  70                  75                  80
117          Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
118                          85                  90                  95
119          Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
120                      100                 105                 110
121          Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
122                      115                 120                 125
123          Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
124              130                 135                 140
125          Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
126          145                 150                 155                 160
127          Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
128                          165                 170                 175
129          Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
130                      180                 185                 190
131          Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
132                      195                 200                 205
133          Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
134              210                 215                 220
135          Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
136          225                 230                 235                 240
137          Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
138                          245                 250                 255
139          Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
140                      260                 265                 270
141          Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
142                      275                 280                 285
143          His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
144              290                 295                 300
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145        Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
146        305                 310                 315                 320
147        His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
148                            325                 330                 335
149        Cys Val Cys Arg Gly Ser Thr Gly Gly
150                            340                 345
151  <210> SEQ ID NO 3
152  <211> LENGTH: 116
153  <212> TYPE: PRT
154  <213> ORGANISM: Artificial Sequence
155  <220> FEATURE:
156  <223> OTHER INFORMATION: peptide motif
157  <220> FEATURE:
158  <221> NAME/KEY: VARIANT
159  <222> LOCATION: (2)...(19)
160  <223> OTHER INFORMATION: Xaa is any amino acid
161  <220> FEATURE:
162  <221> NAME/KEY: VARIANT
163  <222> LOCATION: (20)...(34)
164  <223> OTHER INFORMATION: Xaa is any amino acid or not present
165  <220> FEATURE:
166  <221> NAME/KEY: VARIANT
167  <222> LOCATION: (36)...(36)
168  <223> OTHER INFORMATION: Xaa is any amino acid
169  <220> FEATURE:
170  <221> NAME/KEY: VARIANT
171  <222> LOCATION: (38)...(38)
172  <223> OTHER INFORMATION: Xaa is any amino acid
173  <220> FEATURE:
174  <221> NAME/KEY: VARIANT
175  <222> LOCATION: (40)...(45)
176  <223> OTHER INFORMATION: Xaa is any amino acid
177  <220> FEATURE:
178  <221> NAME/KEY: VARIANT
179  <222> LOCATION: (46)...(72)
180  <223> OTHER INFORMATION: Xaa is any amino acid or not present
181  <220> FEATURE:
182  <221> NAME/KEY: VARIANT
183  <222> LOCATION: (74)...(93)
184  <223> OTHER INFORMATION: Xaa is any amino acid
185  <220> FEATURE:
186  <221> NAME/KEY: VARIANT
187  <222> LOCATION: (94)...(113)
188  <223> OTHER INFORMATION: Xaa is any amino acid not present
189  <220> FEATURE:
190  <221> NAME/KEY: VARIANT
191  <222> LOCATION: (115)...(115)
192  <223> OTHER INFORMATION: Xaa is any amino acid
193  <400> SEQUENCE: 3
194        Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
```

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          195        1              5              10              15
W-->      196     Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          197             20              25              30
W-->      198     Xaa Xaa Cys Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          199          35              40              45
W-->      200     Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          201       50              55              60
W-->      202     Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          203     65              70              75              80
W-->      204     Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          205              85              90              95
W-->      206     Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          207            100             105             110
W-->      208     Xaa Cys Xaa Cys
          209                115
          210     <210> SEQ ID NO 4
          211     <211> LENGTH: 24
          212     <212> TYPE: PRT
          213     <213> ORGANISM: Artificial Sequence
          214     <220> FEATURE:
          215     <223> OTHER INFORMATION: peptide motif
          216     <220> FEATURE:
          217     <221> NAME/KEY: VARIANT
          218     <222> LOCATION: (2)...(2)
          219     <223> OTHER INFORMATION: Xaa is Lys or Arg
          220     <220> FEATURE:
          221     <221> NAME/KEY: VARIANT
          222     <222> LOCATION: (4)...(4)
          223     <223> OTHER INFORMATION: Xaa is Asp, Asn or Glu
          224     <220> FEATURE:
          225     <221> NAME/KEY: VARIANT
          226     <222> LOCATION: (5)...(5)
          227     <223> OTHER INFORMATION: Xaa is Trp, Tyr or Phe
          228     <220> FEATURE:
          229     <221> NAME/KEY: VARIANT
          230     <222> LOCATION: (6)...(16)
          231     <223> OTHER INFORMATION: Xaa is any amino acid
          232     <220> FEATURE:
          233     <221> NAME/KEY: VARIANT
          234     <222> LOCATION: (17)...(20)
          235     <223> OTHER INFORMATION: Xaa is any amino acid or not present
          236     <220> FEATURE:
          237     <221> NAME/KEY: VARIANT
          238     <222> LOCATION: (22)...(22)
          239     <223> OTHER INFORMATION: Xaa is Lys or Arg
          240     <220> FEATURE:
          241     <221> NAME/KEY: VARIANT
          242     <222> LOCATION: (23)...(23)
          243     <223> OTHER INFORMATION: Xaa is Trp, Tyr or Phe
                  <400> SEQUENCE: 4
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/457,066**

Input Set: **I457066.RAW**

Line	?	Error/Warning	Original Text
91	W	Line data has been corrected	Gly Gly *
194	W	"N" or "Xaa" used: Feature required	Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
196	W	"N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
198	W	"N" or "Xaa" used: Feature required	Xaa Xaa Cys Xaa Gly Xaa Cys Xaa Xaa Xaa X
200	W	"N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
202	W	"N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa X
204	W	"N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
206	W	"N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
208	W	"N" or "Xaa" used: Feature required	Xaa Cys Xaa Cys
245	W	"N" or "Xaa" used: Feature required	Cys Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
247	W	"N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Gly Xaa Xaa Cys
270	W	"N" or "Xaa" used: Feature required	atgwsnytnt tyggnytnyt nytnytnacn wsngcnyt
271	W	"N" or "Xaa" used: Feature required	cargcngarw snaayytnws nwsnaartty carttyws
272	W	"N" or "Xaa" used: Feature required	gtncargayc cncarcayga rmgnathath acngtnws
273	W	"N" or "Xaa" used: Feature required	ccnmgnttyc cncayacnta yccnmgnaay acngtnyt
274	W	"N" or "Xaa" used: Feature required	gargaraayg tntggathca rytnacntty gaygarmg
275	W	"N" or "Xaa" used: Feature required	gaygayatht gyaartayga yttygtngar gtngarga
276	W	"N" or "Xaa" used: Feature required	ggnmgntggt gyggnwsngg nacngtnccn ggnaarca
277	W	"N" or "Xaa" used: Feature required	mgnathmgnt tygtnwsnga ygartaytty ccnwsnga
278	W	"N" or "Xaa" used: Feature required	aayathgtna tgccncartt yacngargcn gtnwsncc
279	W	"N" or "Xaa" used: Feature required	ytnccnytng ayytnytnaa yaaygcnath acngcntt
280	W	"N" or "Xaa" used: Feature required	mgntayytng arccngarmg ntggcarytn gayytnga
281	W	"N" or "Xaa" used: Feature required	carytnytng gnaargcntt ygtnttyggn mgnaarws
282	W	"N" or "Xaa" used: Feature required	ytnacngarg argtnmgnyt ntaywsntgy acnccnmg
283	W	"N" or "Xaa" used: Feature required	gargarytna armgnacnga yacnathtty tggccngg
284	W	"N" or "Xaa" used: Feature required	ggnggnaayt gygcntgytg yytncayaay tgyaayga
285	W	"N" or "Xaa" used: Feature required	gtnacnaara artaycayga rgtnytncar ytnmgncc
286	W	"N" or "Xaa" used: Feature required	cayaarwsny tnacngaygt ngcnytngar caycayga
287	W	"N" or "Xaa" used: Feature required	ggnwsnacng gnggn
299	W	"N" or "Xaa" used: Feature required	mgntgyggng gnaaytg
311	W	"N" or "Xaa" used: Feature required	mgntgydsng gnwrytg
323	W	"N" or "Xaa" used: Feature required	carywnccns hrcanck
335	W	"N" or "Xaa" used: Feature required	ttytggccng gntgyyt
347	W	"N" or "Xaa" used: Feature required	ntnddnccnn sntgybt
359	W	"N" or "Xaa" used: Feature required	avrcansnng gnhhnan
379	W	"N" or "Xaa" used: Feature required	caynnnnvnt gyvvntg
391	W	"N" or "Xaa" used: Feature required	canbbrcanb nnnnrtg
403	W	"N" or "Xaa" used: Feature required	tgyacnccnm gnaaytt
415	W	"N" or "Xaa" used: Feature required	tgyhnnmcnm knrmndh
427	W	"N" or "Xaa" used: Feature required	dhnkynmkng knndrca
455	W	"N" or "Xaa" used: Feature required	ywnggnmrnt dbtgygg
467	W	"N" or "Xaa" used: Feature required	ccrcavhany knccnwr
479	W	"N" or "Xaa" used: Feature required	tdbccnmand vntaycc
491	W	"N" or "Xaa" used: Feature required	ggrtanbhnt knggvha
661	W	Line data has been corrected	His Glu Arg Cys Asp Cys Ile Cys Ser Ser A
850	W	Line data has been corrected	Gly *

CORRECTION SUMMARY
PATENT APPLICATION **US/09/457,066**

DATE: 12/22/1999
TIME: 15:03:24

Input Set: **I457066.RAW**

Line	Original Text	Corrected Data
91	Gly Gly *	Gly Gly
661	His Glu Arg Cys Asp Cys Ile Cys Ser Ser A	His Glu Arg Cys Asp Cys Ile Cys Ser Ser A
850	Gly *	Gly